

Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1-8. (Cancelled)

9. (Currently amended) An active site of a ~~C-TRAF2 binding protein or peptide~~ an N-terminal domain of TNFR-1 associated death domain protein (N-TRADD), wherein said active site is characterized by a three dimensional structure comprising the relative structural coordinates of amino acid residues Y16, F18, and H65 according to FIG. 2, \pm a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

10. (Original) The active site of claim 9, wherein the three dimensional structure of said active site further comprises the relative structural coordinates of amino acid residues L17, V58, L59, I72, and D149 according to FIG. 2, \pm a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

11. (Original) The active site of claim 10, wherein the three dimensional structure of said active site further comprises the relative structural coordinates of amino acid residues K63, I64, D68, Q70, V73, Q74, L75, C78, L118, G121, A122, R124, L125, E150, and L152 according to FIG. 2, \pm a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

12. (Original) The active site of claim 10, wherein the root mean square deviation from the conserved backbone atoms of said amino acids is not more than 1.0 Å.

13. (Original) The active site of claim 10, wherein the root mean square deviation from the conserved backbone atoms of said amino acids is not more than 0.5 Å.

14-41. (Cancelled)

42. (New) A three-dimensional model of an N-terminal domain of TNFR-1 associated death domain protein (N-TRADD) active site comprising relative structural coordinates of atoms of an active site of N-TRADD.

43. (New) The model of claim 42, wherein the model includes relative structural coordinates of atoms of amino acid residues Y16, F18, and H65.

44. (New) The model of claim 43, wherein the model further includes relative structural coordinates of atoms of amino acid residues L17, V58, L59, I72, and D149.

45. (New) The model of claim 44, wherein the model further includes relative structural coordinates of atoms of amino acid residues K63, I64, D68, Q70, V73, Q74, L75, C78, L118, G121, A122, R124, L125, E150, and L152.

46. (New) The model of claim 42, wherein the relative structural coordinates are according to FIG. 2, \pm a root mean square deviation for conserved backbone atoms of amino acid residues of not more than 1.5 Å.

47. (New) The model of claim 46, wherein the root mean square deviation for conserved backbone atoms of amino acid residues is not more than 1.0 Å.

48. (New) The model of claim 46, wherein the root mean square deviation for conserved backbone atoms of said amino acids is not more than 0.5 Å.

49. (New) A machine readable storage medium comprising a data storage material encoded with machine readable data, the machine readable data comprising relative structural coordinates of atoms of an N-terminal domain of TNFR-1 associated death domain protein (N-TRADD).

50. (New) The machine readable storage medium of claim 49, wherein the relative structural coordinates include relative structural coordinates of atoms of amino acid residues Y16, F18, and H65.

51. (New) The machine readable storage medium of claim 50, wherein the relative structural coordinates further include relative structural coordinates of atoms of amino acid residues L17, V58, L59, I72, and D149.

52. (New) The machine readable storage medium of claim 51, wherein the relative structural coordinates further include relative structural coordinates of atoms of amino acid residues K63, I64, D68, Q70, V73, Q74, L75, C78, L118, G121, A122, R124, L125, E150, and L152.

53. (New) The machine readable storage medium of claim 49, wherein the relative structural coordinates are according to FIG. 2, \pm a root mean square deviation for conserved backbone atoms of amino acid residues of not more than 1.5 Å.

54. (New) The machine readable storage medium of claim 53, wherein the root mean square deviation for conserved backbone atoms of amino acid residues is not more than 1.0 Å.

55. (New) The machine readable storage medium of claim 53, wherein the root mean square deviation for conserved backbone atoms of amino acid residues is not more than 0.5 Å.

56. (New) A computer system comprising:
a central processing unit;
a machine readable storage medium operably connected to the central processing unit, comprising a data storage material encoded with machine readable data, the machine readable data comprising relative structural coordinates of atoms of an N-terminal domain of TNFR-1 associated death domain protein (N-TRADD); and
a display operably connected to the central processing unit, wherein the central processing unit is programmed with instructions for displaying on the display a three-dimensional model of the N-terminal domain of TNFR-1 associated death domain protein according to the relative structural coordinates.

57. (New) The computer system of claim 56, wherein the relative structural coordinates include relative structural coordinates of atoms of amino acid residues Y16, F18, and H65.

58. (New) The computer system of claim 57, wherein the relative structural coordinates further include relative structural coordinates of atoms of amino acid residues L17, V58, L59, I72, and D149.

59. (New) The computer system of claim 58, wherein the relative structural coordinates further include relative structural coordinates of atoms of amino acid residues K63, I64, D68, Q70, V73, Q74, L75, C78, L118, G121, A122, R124, L125, E150, and L152.

60. (New) The computer system of claim 56, wherein the relative structural coordinates are according to FIG. 2, \pm a root mean square deviation for conserved backbone atoms of amino acid residues of not more than 1.5 Å.

61. (New) The computer system of claim 60, wherein the root mean square deviation for conserved backbone atoms of amino acid residues is not more than 1.0 Å.

62. (New) The computer system of claim 61, wherein the root mean square deviation for conserved backbone atoms of amino acid residues is not more than 0.5 Å.